CURRENT STATUS OF ALL CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application.

1. (original) A method of detecting typable loci of a genome, comprising the steps of:

(a) providing an amplified representative population of genome fragments comprising said typable loci, wherein said population comprises a high complexity representation;

(b) contacting said genome fragments with a plurality of nucleic acid probes having sequences corresponding to said typable loci under conditions wherein probe-fragment hybrids are formed, wherein said probes are at most 125 nucleotides in length; and

(c) detecting typable loci of said probe-fragment hybrids.

2. (original) The method of claim 1, wherein said population of representative genome fragments comprises sequences identical to at least 5% of the genome.

3. (original) The method of claim 1, wherein said providing in step (a) comprises representationally amplifying a native genome.

4. (original) The method of claim 3, wherein said representationally amplifying comprises using a polymerase of low processivity.

5. (original) The method of claim 3, wherein said low processivity is less than 100 bases per polymerization event.

6. (original) The method of claim 3, wherein said representationally amplifying comprises a single step reaction yielding a high complexity representation.

7. (original) The method of claim 3, wherein at most 1×10^6 copies of said native genome are used as a template for amplification.

8. (original) The method of claim 1, wherein said nucleic acid probes are immobilized on a substrate.

9. (original) The method of claim 8, wherein said substrate is selected from the group consisting of a particle, bead, surface, slide, and microchip.

10. (original) The method of claim 1, wherein at least 100 typable loci are simultaneously detected.

11. (original) The method of claim 1, wherein said genome is a human genome.

12. (original) The method of claim 1, wherein step (b) comprises contacting said genome fragments with a multiplexed array of nucleic acid probes.

13. (original) The method of claim 1, further comprising contacting said array of nucleic acid probes with chaperone probes.

14. (original) The method of claim 1, wherein said probes comprise nucleic acid probes that are at least 20 nucleotides in length.

15. (original) The method of claim 1, further comprising producing a report identifying said typable loci that are detected.

16. (original) A report produced by the method of claim 15.

17. (original) The method of claim 1, wherein step (c) comprises directly detecting said typable loci of said fragments that hybridize to said probes.

18. (original) A method of detecting typable loci of a genome, comprising the steps of:

(a) providing an amplified representative population of genome fragments comprising said typable loci;

(b) contacting said genome fragments with a plurality of nucleic acid probes having sequences corresponding to said typable loci under conditions wherein probe-fragment hybrids are formed; and

(c) directly detecting typable loci of said probe-fragment hybrids

19. (original) The method of claim 18, wherein at most 1000 copies of said native genome are amplified.

20. (original) The method of claim 18, wherein said population of representative genome fragments comprises sequences identical to at least 60% of the genome.

21. (original) The method of claim 18, wherein said plurality of nucleic acid probes has sequences for typable loci linked to at least 5% of the expressed sequences of said genome.

22. (original) The method of claim 18, wherein said providing in step (a) comprises representationally amplifying a native genome.

23. (original) The method of claim 22, wherein said representationally amplifying comprises using a polymerase of low processivity.

24. (original) The method of claim 22, wherein said low processivity is less than 100 bases per polymerization event.

25. (original) The method of claim 22, wherein said representationally amplifying comprises a single step reaction yielding a high complexity representation.

26. (original) The method of claim 22, wherein at most 1×10^6 copies of said native genome are used as a template for amplification.

27. (original) The method of claim 18, wherein said nucleic acid probes are immobilized on a substrate.

28. (original) The method of claim 18, wherein said substrate is selected from the group consisting of a particle, bead, surface, slide, and microchip.

29. (original) The method of claim 18, wherein at least 100 typable loci are simultaneously detected.

30. (original) The method of claim 18, wherein said genome is a human genome.

31. (original) The method of claim 18, wherein step (b) comprises contacting said genome fragments with a multiplexed array of nucleic acid probes.

32. (original) The method of claim 31, further comprising contacting said array of nucleic acid probes with chaperone probes.

33. (original) The method of claim 18, wherein said probes comprise nucleic acid probes are at least 20 nucleotides in length.

34. (original) The method of claim 2, further comprising producing a report identifying said typable loci that are detected.

35. (original) A report produced by the method of claim 34.

36. (original) The method of claim 18, wherein step (c) comprises directly detecting said typable loci of said fragments that hybridize to said probes.

37. (original) A method of detecting typable loci of a genome, comprising the steps of:

(a) providing an amplified representative population of genome fragments comprising said typable loci;

(b) contacting said genome fragments with a plurality of immobilized nucleic acid probes having sequences corresponding to said typable loci under conditions wherein immobilized probe-fragment hybrids are formed;

(c) modifying said immobilized probe-fragment hybrids; and

(d) detecting a probe or fragment modified in step (c), thereby detecting said typable loci of said genome.

38. (original) The method of claim 37, wherein said plurality of nucleic acid probes has sequences for typable loci linked to at least 10% of the expressed sequences of said genome.

39. (original) The method of claim 37, wherein said providing in step (a) comprises representationally amplifying a native genome.

40. (original) The method of claim 39, wherein said representationally amplifying comprises using a polymerase of low processivity.

41. (original) The method of claim 39, wherein said low processivity is less than 100 bases per polymerization event.

42. (original) The method of claim 39, wherein said representationally amplifying comprises a single step reaction yielding a high complexity representation.

43. (original) The method of claim 39, wherein at most 1×10^6 copies of said native genome are used as a template for amplification.

44. (original) The method of claim 37, wherein said nucleic acid probes are immobilized on a substrate.

45. (original) The method of claim 44, wherein said substrate is selected from the group consisting of a particle, bead, surface, slide, and microchip.

46. (original) The method of claim 37, wherein at least 100 typable loci are simultaneously detected.

47. (original) The method of claim 37, wherein said genome is a human genome.

48. (original) The method of claim 37, wherein step (b) comprises contacting said genome fragments with a multiplexed array of nucleic acid probes.

49. (original) The method of claim 48, further comprising contacting said array of nucleic acid probes with chaperone probes.

50. (original) The method of claim 37, wherein said probes comprises nucleic acid probes are at least 20 nucleotides in length.

51. (original) The method of claim 37, further comprising producing a report identifying said typable loci that are detected.

52. (original) A report produced by the method of claim 51.

53. (original) The method of claim 37, wherein step (c) comprises a primer extension assay.

54. (original) The method of claim 53, wherein said primer extension assay is selected from the group consisting of allele specific primer extension (ASPE), single base extension (SBE) and pyrosequencing.

Claims 55-77 (cancelled).

78. (New) A method of detecting typable loci of a genome, comprising

(a) contacting a plurality of genome fragments with a plurality of different immobilized nucleic acid probes under conditions wherein immobilized probe-fragment hybrids are formed;

(b) modifying said immobilized probe-fragment hybrids by addition of a detection moiety to the probe, thereby forming affinity ligand-labeled probes;

(c) contacting said affinity ligand-labeled probes with a binding moiety and an amplification reagent,

wherein said binding moiety has one or more sites capable of binding said ligand, and wherein said amplification reagent has affinity for said binding moiety,

whereby a multimeric complexes form between said affinity ligand-labeled probe, said binding moiety and said amplification reagent; and

(d) detecting said multimeric complexes, thereby detecting typable loci of said genome fragments.

79. (new) The method of claim 78, wherein said plurality of different immobilized nucleic acid probes comprises an array of said probes attached to a surface.

80. (new) The method of claim 78, wherein said plurality of different immobilized nucleic acid probes are attached to particles.

81. (new) The method of claim 80, wherein each of said particles is attached to a single type of nucleic acid probe.

82. (new) The method of claim 80, wherein said particles are attached to a substrate.

83. (new) The method of claim 78, wherein at least 100,000 of said different immobilized nucleic acid probes hybridize with genome fragments to form said immobilized probe-fragment hybrids.

84. (new) The method of claim 78, wherein said modifying comprises addition of a nucleotide or nucleotide analog comprising said detection moiety.

85. (new) The method of claim 78, wherein said modifying comprises ligation of probes to said immobilized nucleic acid probes, wherein said probes comprise said detection moiety.

86. (new) The method of claim 78, further comprising contacting said probes with a single-stranded nucleic acid binding protein.

87. (new) The method of claim 78, wherein at least 100 typable loci are simultaneously detected.